

RAW SEQUENCE LISTING

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Application Serial Number: 09/485,650
Source: IPW16
Date Processed by STIC: 8/22/05

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IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/485,650

DATE: 08/22/2005
TIME: 08:33:16

Input Set : A:\Cml817.app
Output Set: N:\CRF4\08222005\I485650.raw

3 <110> APPLICANT: Bettiol, Jean-Luc P.
 4 Thoen, Christiaan AJK
 6 <120> TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a
 7 Soil Release Polymer
 9 <130> FILE REFERENCE: Mannanase and soil release polymer
 11 <140> CURRENT APPLICATION NUMBER: 09/485,650
C--> 12 <141> CURRENT FILING DATE: 2000-04-05
 14 <150> PRIOR APPLICATION NUMBER: PCT/US98/12027
 15 <151> PRIOR FILING DATE: 1998-06-10
 17 <160> NUMBER OF SEQ ID NOS: 6
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1482
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bacillus sp.
 26 <400> SEQUENCE: 1
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 28 ggaataatgg ggattacaac gtccccatca gcagoaagta caggcttta tggtgatggc 120
 29 aatacgttat atgacgc当地 tggcgagcca tttgtcatga gaggtattaa ccatggacat 180
 30 gcttggata aagacaccgc ttcaacagct attccgttcca ttgcagagca aggcccaac 240
 31 acgattcgtt atgttttatac agatggcggt caatggaaa aagacgacat tgacaccatt 300
 32 cgtgaagtca ttgagcttgc ggagcaaaat aaaatggtgg ctgtcggtga agttcatgtat 360
 33 gccacgggtc gcgattcgc当地 cagtgttta aatcgagccg ttgattattt gataaaaaatg 420
 34 aaagatgc当地 ttatcggtaa agaagatacg gttattattt acattgcaaa cgagtggat 480
 35 gggagttggg atggctcgc当地 ttggccgat ggctatattt atgtcatttc gaagcttcgc 540
 36 gatgccggct taacacacac cttaatgggt gatgcagcag gatgggggca atatccgcaa 600
 37 tctattcatg attacggaca agatgtgtt aatcgagatc cgtaaaaaaaa tacgtatgtt 660
 38 tccatccata tgtatgagta tgctgggtt gatgctaaca ctgttagatc aaatattgtat 720
 39 agagtcatag atcaagaccc tgcgtcgta ataggtgaat tcggcatag acataactgtat 780
 40 ggtgatgtt atgaagatac aatccttagt tattctgaag aaactggcac agggtggctc 840
 41 gcttggctt ggaaaggcaa cagtaccgaa tgggactatt tagaccttcc agaagactgg 900
 42 gctggtaaac atttaactga ttggggaaat agaattgtcc acggggccga tggcttacag 960
 43 gaaacctcca aaccatccac cgtatttaca gatgataacg gtggtcaccc tgaaccgcca 1020
 44 actgctacta cttgtatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg 1080
 45 accggtgccc cttggccgt aacagaatgg ggtgcttc当地 gtaactactc tttaaaagcc 1140
 46 gatgtaaatt taacctcaa ttcttc当地 gtaactgtata gtgaacaaag tcgtatctca 1200
 47 cacggatact ctcagctcaa cgcaaccgtt cgccatgcca attggggaaa tcccggtaat 1260
 48 ggc当地 gaatg caagacttta cgtgaaaacg ggctctgatt atacatggca tagcggccct 1320
 49 tt当地 acacgttcaatacgcttcaactc当地 agaactgtt ctttgattt aaacaacatc 1380
 50 gaaaatagtc atcatgttag ggaaataggc gtgcaatttt cagcggcaga taatagcagt 1440
 51 ggtcaaactg ctctatacgt tgataacgtt actttaagat ag 1482
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 493

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56 <212> TYPE: PRT
 57 <213> ORGANISM: Bacillus sp.
 59 <400> SEQUENCE: 2
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 20 25 30
 66 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
 35 40 45
 69 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
 50 55 60
 72 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
 65 70 75 80
 75 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
 85 90 95
 78 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
 100 105 110
 81 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
 115 120 125
 84 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
 130 135 140
 87 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
 145 150 155 160
 90 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
 165 170 175
 93 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
 180 185 190
 96 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
 195 200 205
 99 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
 210 215 220
 102 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
 225 230 235 240
 105 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
 245 250 255
 108 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
 260 265 270
 111 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
 275 280 285
 114 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
 290 295 300
 117 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
 305 310 315 320
 120 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
 325 330 335
 123 Pro Glu Pro Pro Thr Ala Thr Leu Tyr Asp Phe Glu Gly Ser Thr
 340 345 350
 126 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
 355 360 365

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129 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
130      370          375          380
132 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
133      385          390          395          400
135 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
136          405          410          415
138 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
139          420          425          430
141 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
142          435          440          445
144 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His
145          450          455          460
147 His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser
148          465          470          475          480
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151          485          490
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 1407
156 <212> TYPE: DNA
157 <213> ORGANISM: Bacillus sp.
159 <400> SEQUENCE: 3
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161 ggaataatgg ggattacaac gtcccccata gcagcaagta caggcttta tggatggc 120
162 aatacggtat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
163 gcttggata aagacaccgc ttcaacagct attcctgccca ttgcagagca aggcccaac 240
164 acgattcgta ttgtttatc agatggcggt caatggaaa aagacgacat tgacaccatt 300
165 cgtgaagtca ttgagcttgc ggagaaaaat aaaatggtgg ctgtcgatg agttcatgat 360
166 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattt gatagaaatg 420
167 aaagatgcgc ttatcgtaa agaagatacg gttattatta acattgcaaa cgagtggat 480
168 gggagttggg atggctcagc ttggccgat ggctatattt atgtcatcc gaagcttcgc 540
169 gatgccggct taacacacac cttaatggtt gatcagcag gatggggca atatccgcaa 600
170 tctattcatg attacggaca agatgtgtt aatgcagatc cgtaaaaaaa tacatgttc 660
171 tccatccata tgtatgagta tgctgggtt gatgctaaca ctgttagatc aaatattgat 720
172 agagtcatac atcaagaccc tgcgtcgta ataggtaat tcggcatag acatactgat 780
173 ggtgatgtt atgaagatac aatccttagt tattctgaag aaactggcac agggtggctc 840
174 gcttggtctt ggaaaggcaa cagtaccgaa tgggactatt tagaccttc agaagactgg 900
175 gctggtaaac attaactga ttggggaaat agaattgtcc acggggccga tggcttacag 960
176 gaaacctcca aaccatccac cgtatattaca gatgataacg gtggcacccc tgaaccgcca 1020
177 actgctacta ctttgatga ctttgaagga agcacacaaag ggtggcatgg aagcaacgtg 1080
178 accgggtggcc cttggccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc 1140
179 gatgtaaatt taacctaaaa ttcttcacat gaaactgtata gtgaacaaag tcgtaatcta 1200
180 cacggatact ctcagctaa cgcaaccgtt cgccatgccca attggggaaa tcccgtaat 1260
181 ggcataatg caagacttta cgtaaaaacg ggctctgatt atacatggca tagcggtcct 1320
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186 <210> SEQ ID NO: 4
187 <211> LENGTH: 468
188 <212> TYPE: PRT
189 <213> ORGANISM: Bacillus sp.

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196   20          25           30
198 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
199   35          40           45
201 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
202   50          55           60
204 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
205   65          70           75           80
207 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
208   85          90           95
210 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
211   100         105          110
213 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
214   115         120          125
216 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
217   130         135          140
219 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
220   145         150          155          160
222 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
223   165         170          175
225 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
226   180         185          190
228 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
229   195         200          205
231 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
232   210         215          220
234 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
235   225         230          235          240
237 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
238   245         250          255
240 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
241   260         265          270
243 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
244   275         280          285
246 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
247   290         295          300
249 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
250   305         310          315          320
252 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
253   325         330          335
255 Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr
256   340         345          350
258 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
259   355         360          365
261 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
262   370         375          380

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264 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
265 385 390 395 400
267 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
268 405 410 415
270 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
271 420 425 430
273 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
274 435 440 445
276 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ile Ile
277 450 455 460
279 Met Leu Gly Lys
280 465
283 <210> SEQ ID NO: 5
284 <211> LENGTH: 1029
285 <212> TYPE: DNA
286 <213> ORGANISM: Bacillus sp.
288 <400> SEQUENCE: 5
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291 gaggttacag ccatgacaca ttttctatgg ctgaggctga tagaatccga agcgccaccg 180
292 ggcaatcgcc tgcttattt ggctgcgatt atgcagagg atggcttgaa acagcaaata 240
293 ttgaagattc aatagatgta agctgcaacg gcgatttaat gtcgtattgg aaaaatggcg 300
294 gaattccgca aatcagttt cacctggcga accctgctt tcagtcaggg cattttaaaa 360
295 caccgattac aaatgatcag tataaaaaca tattagattc agcaacagcg gaaggaaagc 420
296 ggctaaatgc catgctcagc aaaattgctg acggacttca agagttggag aaccaaggtg 480
297 tgcctgttct gttcaggccg ctgcatgaaa tgaacggcga atggtttgg tggggactca 540
298 catcatataa ccaaaaaggat aatgaaagaa tctctctata taaacagctc tacaagaaaa 600
299 tctatcatta tatgaccgac acaagaggac ttgatcattt gatttgggtt tactctcccg 660
300 acgccaaccg agattttaaa actgatttt accccggcgc gtcttacgtg gatattgtcg 720
301 gattagatgc gtatttcaa gatgcctact cgatcaatgg atacgatcag ctaacagcgc 780
302 ttaataaacc atttgctttt acagaagtcg gcccggaaac agcaaacggc agtttcgatt 840
303 acagcctgtt catcaatgca ataaaacaaa aatatcctaa aaccatttac ttctggcat 900
304 ggaatgatga atggagcgcgca gcagtaaaca agggtgctt agctttatat catgacagct 960
305 ggacactcaa caagggagaa atatggaatg gtgattctt aacgccaatc gttgagtgaa 1020
306 tccgggatc 1029
309 <210> SEQ ID NO: 6
310 <211> LENGTH: 362
311 <212> TYPE: PRT
312 <213> ORGANISM: Bacillus sp.
314 <400> SEQUENCE: 6
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318 Ser Ala Val Leu Ala Lys Pro Ile Glu Ala His Thr Val Ser Pro Val
319 20 25 30
321 Asn Pro Asn Ala Gln Gln Thr Thr Lys Thr Val Met Asn Trp Leu Ala
322 35 40 45
324 His Leu Pro Asn Arg Thr Glu Asn Arg Val Leu Ser Gly Ala Phe Gly
325 50 55 60
327 Gly Tyr Ser His Asp Thr Phe Ser Met Ala Glu Ala Asp Arg Ile Arg

VERIFICATION SUMMARY

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